FIG.1

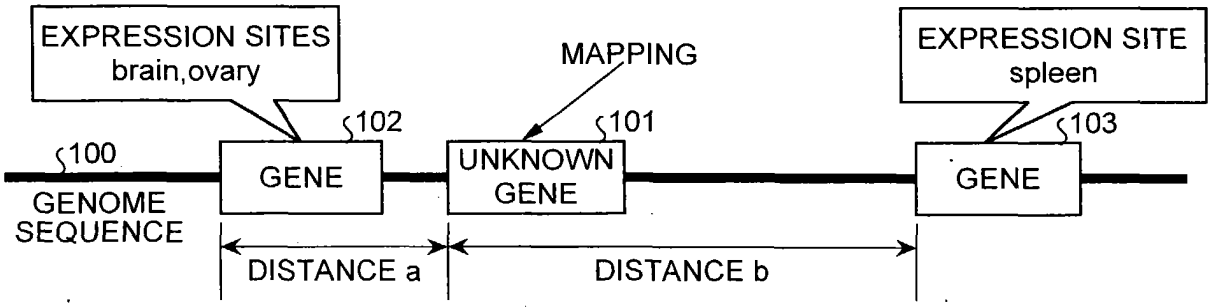
EXPRESSION SITES
brain,ovary
MAPPING
EXPRESSION SITE
spleen
102
101
103
100
GENE
UNKNOWN
GENE
GENE
GENOME
SEQUENCE
DISTANCE a
DISTANCE b

FIG.2

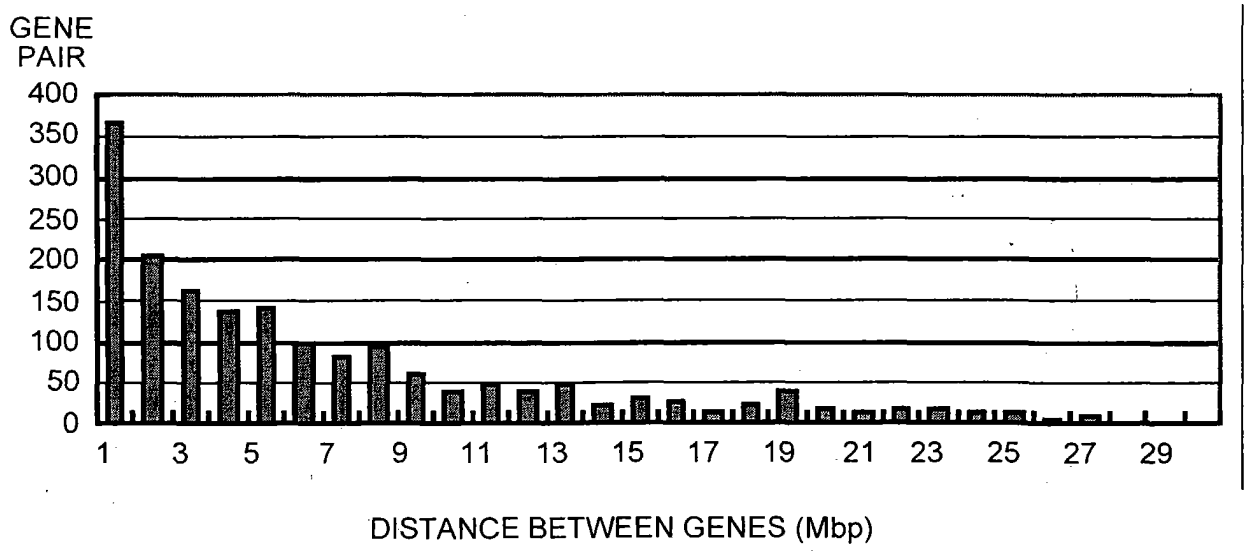
GENE
PAIR
400
350
300
250
200
150
100
50
0
1
3
5
7
9
11
13
15
17
19
21
23
25
27
29
DISTANCE BETWEEN GENES (Mbp)

FIG.3

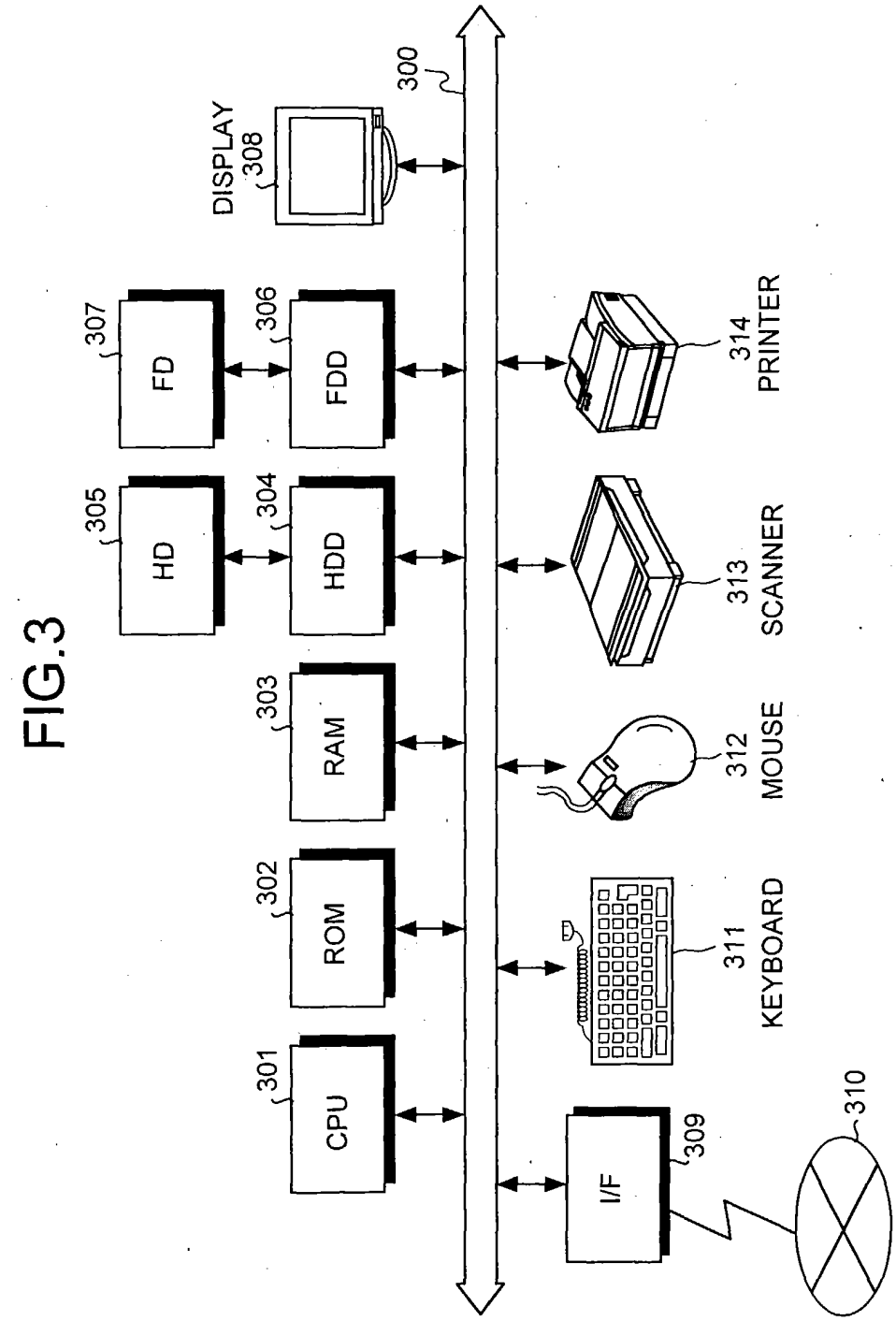
300
DISPLAY
308
FD
307
FDD
306
HD
305
HDD
304
RAM
303
ROM
302
CPU
301
I/F
309
310
311
KEYBOARD
312
MOUSE
313
SCANNER
314
PRINTER

FIG.4

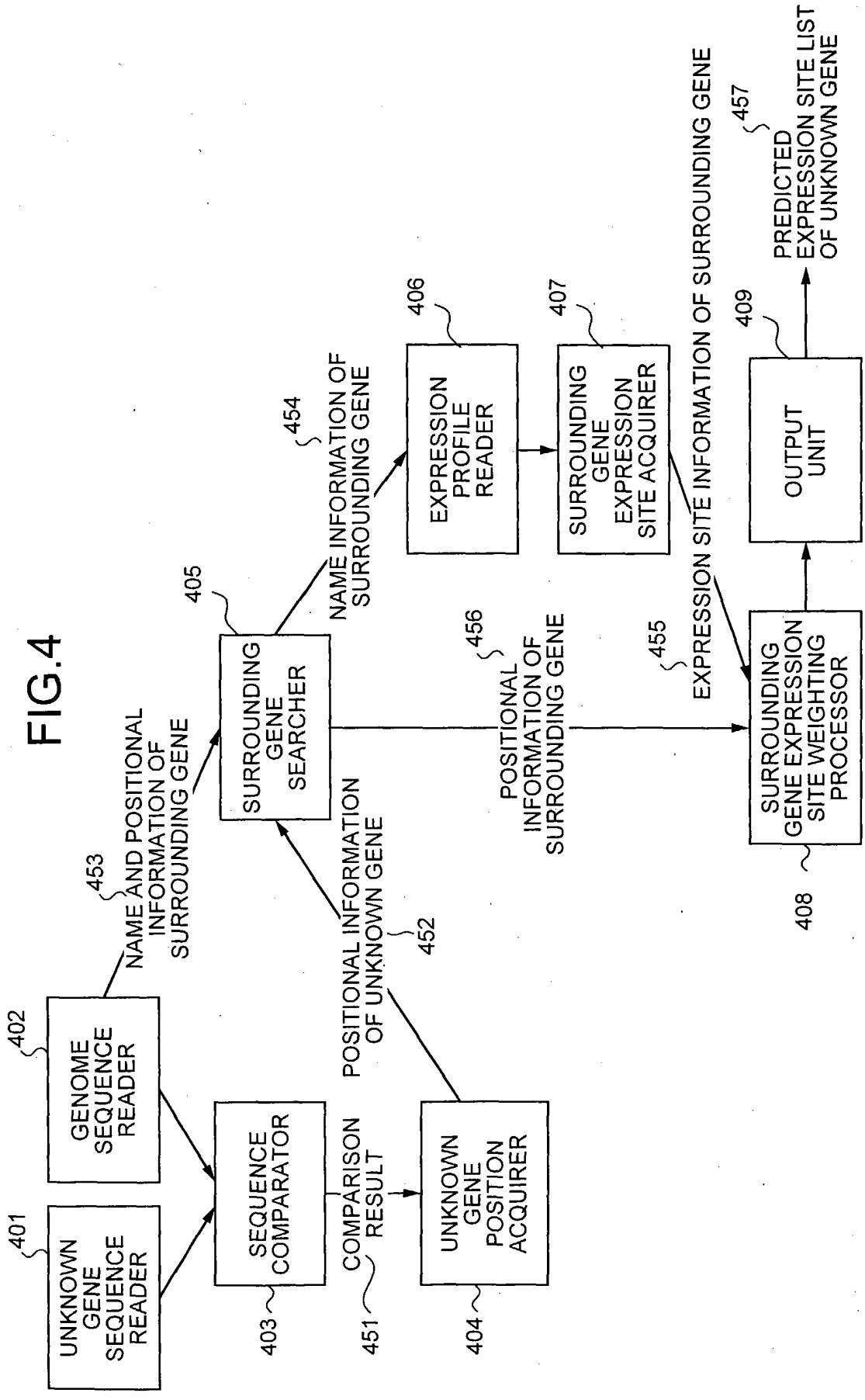
UNKNOWN GENE SEQUENCE READER
401
GENOME SEQUENCE READER
402
SEQUENCE COMPARATOR
403
UNKNOWN GENE POSITION ACQUIRER
404
SURROUNDING GENE SEARCHER
405
EXPRESSION PROFILE READER
406
SURROUNDING GENE EXPRESSION SITE ACQUIRER
407
SURROUNDING GENE EXPRESSION SITE WEIGHTING PROCESSOR
408
OUTPUT UNIT
409
NAME AND POSITIONAL INFORMATION OF SURROUNDING GENE
453
POSITIONAL INFORMATION OF UNKNOWN GENE
452
COMPARISON RESULT
451
NAME INFORMATION OF SURROUNDING GENE
454
POSITIONAL INFORMATION OF SURROUNDING GENE
456
EXPRESSION SITE INFORMATION OF SURROUNDING GENE
455
PREDICTED EXPRESSION SITE LIST OF UNKNOWN GENE
457

FIG.5

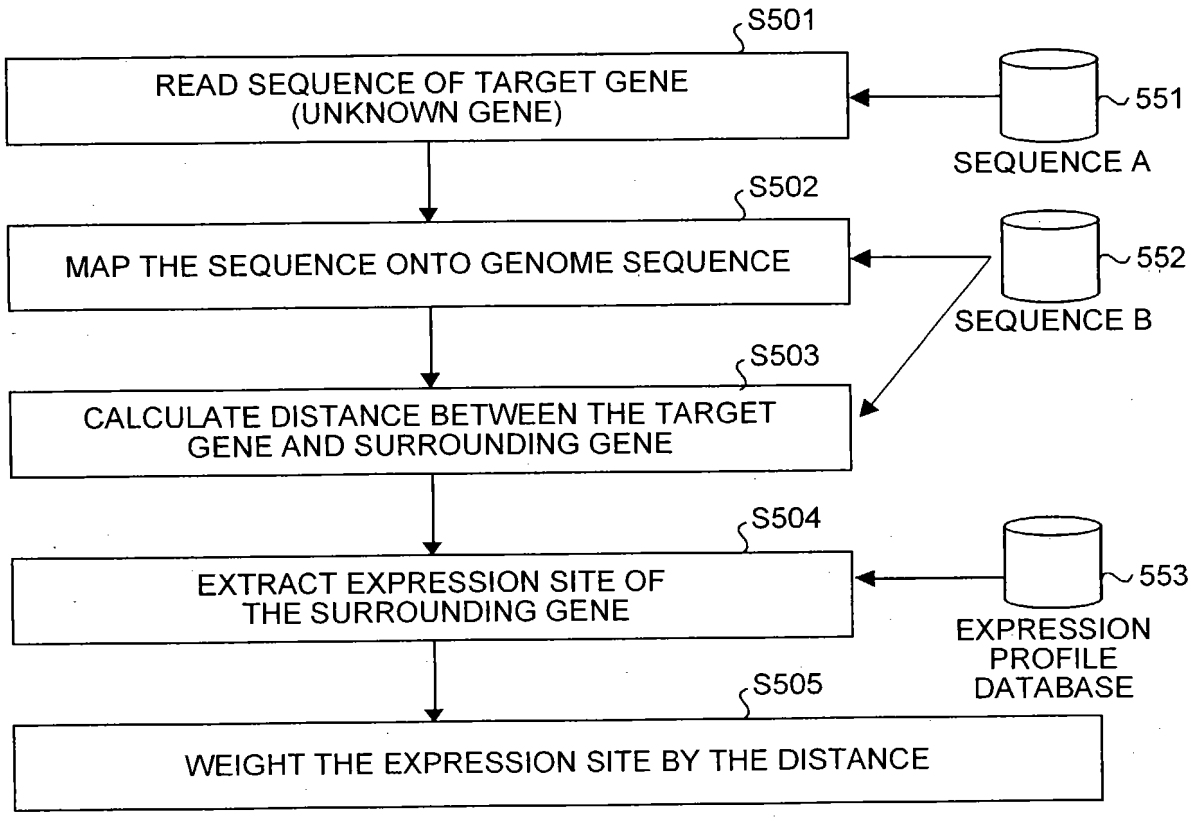
S501
READ SEQUENCE OF TARGET GENE (UNKNOWN GENE)
551
SEQUENCE A
S502
MAP THE SEQUENCE ONTO GENOME SEQUENCE
552
SEQUENCE B
S503
CALCULATE DISTANCE BETWEEN THE TARGET GENE AND SURROUNDING GENE
S504
EXTRACT EXPRESSION SITE OF THE SURROUNDING GENE
553
EXPRESSION PROFILE DATABASE
S505
WEIGHT THE EXPRESSION SITE BY THE DISTANCE

FIG.6

551

GGCTGCCGAAGATGGCGGAGGTGCAGGTCCTGGTGCTCGATGGTCGAGGCCATCTCCTGGTCCGCCTGGC
GGCCATCGTGGCTAAACAGGTACTGCTGGGCCGGAAAGTGGTGGTCGTACGCTGCGAAGGCATCAACATT
TCTGGCAATTTCTACAGAAACAAGTTGAAGTACCTGGGTTTCCTCCGCAAGCGGATGAACACCCACCTTT
CCCGAGGTCCCTACCACTTCCGGGCCCCCCAGCCGCATCTTCTGGCGGACCGTGCGAGGTATGCCGCCCC
ACAAGACCAAGCGAGGCCAGGCTTCTCTGGACCGCCTCAAGGTGTTTGACCGCATCCCACCGCCCTACGA
CAAGAAAAAGCGGATGCTGGAAGTACCAGGCAGTGACAGCCACCCTGGAGGAGAAGAGGAAAGAGAAAGC
CA

FIG.7

552

. . . . . .

TATTCTCTTAGCTTGTGTTGGCCAATTGTTTGCTTATGGGGGAATGACTTTTGAAGACTTGATCTAGAGA
TGGAATCCACAGTCCTCTTTCTCATTTCATCCAAACTGAGTCTGCTGTTTTGTGTTTTATTTATAGAGCA
GTCAGGTTCCTTTCTTCCCTGAAGCCAACCTAGTACCTAGGGCACTAAGATTATGTTAAGAGGCTTTTGT
GTGCTAATGTGCTAATTCAAGGCTGATGGAAGTGAATTTTTATCATAATAATGTGAATAAAATACATTTT
TCTGAAAAAAAAAAGTGAGTTCTCACCAAAACCAGTGGAAGGAGCCCATGATCCACCAAACAGGGACTTC
TCAGCTACAAATGGGAACGTTTGTGTCTCCAGCTGGGCTGCAGCTCCACCTGCAGAATGAGGAGGAAGGG
ACCACAAAGTAAACAGGTGATAGTCATTACTAACATTTCCATCATCTGCTTTTCCTCTCAATGGCCAGTT
AACACAAGATGTCCTCTTGCACAGATGCAGAATCTCATAAGCCATCAACTTTACCCTGAATAGAAGTAAA
AAGGTCTTTATTCATTTTTCCTCCCCCCTAAATTTATTAAATACCTGATAGATGTCAAACACTGTTAGGT
ATGAAGATACAGTCATGAGTGAAGCATGTTCTTGGAAAGAAGACATAGCCCAGCTCTCCATAGAAATGAA
ATACAGCAATAATATATGTATTTATAATAGGTTAATGGGTTTTTTTGTCTACAAAAAAAAACAAATTTTT
CTATCACTTAGCAAAGTGACTAGGTCATTTTACTTTTTTGAACTTGATTATTTGGCTAATATTATAAAAT
GCCAGAGCTAAAAATAGCTGTACCTGGGGTGAAATGGAGAAGACGTGGGACATAGCTTTAAAAATGGGAG
AAGCGCTTTTTCCCAAGCGGCTGCCGAAGATGGCGGAGGTGCAGGTCCTGGTGCTCGATGGTCGAGGCCA
TCTCCTGGTCCGCCTGGCGGCCATCGTGGCTAAACAGGTACTGCTGGGCCGGAAAGTGGTGGTCGTACGC
TGCGAAGGCATCAACATTTCTGGCAATTTCTACAGAAACAAGTTGAAGTACCTGGGTTTCCTCCGCAAGC
GGATGAACACCCACCTTTCCCGAGGTCCCTACCACTTCCGGGCCCCCCAGCCGCATCTTCTGGCGGACCG
TGCGAGGTATGCCGCCCCACAAGACCAAGCGAGGCCAGGCTTCTCTGGACCGCCTCAAGGTGTTTGACCG
CATCCCACCGCCCTACGACAAGAAAAAGCGGATGGTGTTCCTGCTCCCTCAAGGTTGTGCGTCTGAAGCC
TACAAGAAAGTTTGCCTATCTGGGGCGCCTGGCTCACGAGGTTGGCTGGAAGTACCAGGCAGTGACAGCC
ACCCTGGAGGAGAAGAGGAAAGAGAAAGCCAAGATCCACTACCGGAAGAAGAAACAGCTCATGAGGCTAC

. . . . . .

FIG.8


SEQUENCE B TAAGCCATCAACTTTACCCTGAATAGAAGTAAAAAGGTCTTTATTCATTTTTCCTCCCCC 12313447
SEQUENCE A
802
SEQUENCE B GGACATAGCTTTAAAAATGGGAGAAGCGCTTTTTCCCAAGCGGCTGCCGAAGATGGCGGA 12313807
SEQUENCE A GGCTGCCGAAGATGGCGGA 19
SEQUENCE B GGTGCAGGTCCTGGTGCTCGATGGTCGAGGCCATCTCCTGGTCCGCCTGGCGGCCATCGT 12313867
SEQUENCE A GGTGCAGGTCCTGGTGCTCGATGGTCGAGGCCATCTCCTGGTCCGCCTGGCGGCCATCGT 79
SEQUENCE B GGCTAAACAGGTACTGCTGGGCCGGAAAGTGGTGGTCGTACGCTGCGAAGGCATCAACAT 12313927
SEQUENCE A GGCTAAACAGGTACTGCTGGGCCGGAAAGTGGTGGTCGTACGCTGCGAAGGCATCAACAT 139
SEQUENCE B TTCTGGCAATTTCTACAGAAACAAGTTGAAGTACCTGGGTTTCCTCCGCAAGCGGATGAA 12313987
SEQUENCE A TTCTGGCAATTTCTACAGAAACAAGTTGAAGTACCTGGGTTTCCTCCGCAAGCGGATGAA 199
SEQUENCE B CACCCACCTTTCCCGAGGTCCCTACCACTTCCGGGCCCCCCAGCCGCATCTTCTGGCGGA 12314047
SEQUENCE A CACCCACCTTTCCCGAGGTCCCTACCACTTCCGGGCCCCCCAGCCGCATCTTCTGGCGGA 259
SEQUENCE B CCGTGCGAGGTATGCCGCCCCACAAGACCAAGCGAGGCCAGGCTTCTCTGGACCGCCTCA 12314107
SEQUENCE A CCGTGCGAGGTATGCCGCCCCACAAGACCAAGCGAGGCCAGGCTTCTCTGGACCGCCTCA 319
SEQUENCE B AGGTGTTTGACCGCATCCCACCGCCCTACGACAAGAAAAAGCGGATGGTGTTCCTGCTCC 12314167
SEQUENCE A AGGTGTTTGACCGCATCCCACCGCCCTACGACAAGAAAAAGCGGATG 379
SEQUENCE B CTCAAGGTTGTGCGTCTGAAGCCTACAAGAAAGTTTGCCTATCTGGGGCGCCTGGCTCAC 12314227
SEQUENCE A
801
SEQUENCE B GAGGTTGGCTGGAAGTACCAGGCAGTGACAGCCACCCTGGAGGAGAAGAGGAAAGAGAAA 12314287
SEQUENCE A CTGGAAGTACCAGGCAGTGACAGCCACCCTGGAGGAGAAGAGGAAAGAGAAA 418
SEQUENCE B GCCAAGATCCACTACCGGAAGAAGAAACAGCTCATGAGGCTACGGAAACAGGCCGAGAAG 12314347
SEQUENCE A GCCA 422

FIG.9

SUR-ROUNDING GENE NAME	POSITION (bp)
ABCC13	1311191
STCH	1410233
SAMSN1	1522621
NRIP1	1998612
USP25	2767504
CXADR	4550321
BTG3	4630946
C21orf91	4826288
C21orf68	5282143
PRSS7	5306683
NCAM2	8232571
C21orf42	12337804
MRPL39	12537621
JAM2	12591245
ATP5J	12676442
GABPA	12681637
APP	12832513
CYYR1	13418319
ADAMTS1	13788256
ADAMTS5	13873414
N6AMT1	15824387
ZNF294	15880030
C21orf6	15957644
USP16	15976534
CCT8	16008212
C21orf7	16027963
BACH1	16249331
GRIK1	16487389
CLDN17	17116394
CLDN8	17164457
TIAM1	18068878
SOD1	18610012

SUR-ROUNDING GENE NAME	POSITION (bp)
KIAA1172	18621440
HUNK	18823719
C21orf45	19219355
C21orf108	19261422
MGC14136	19343534
C21orf63	19362789
FLJ10932	19522641
C21orf59	19552201
SYNJ1	19579165
C21orf66	19706745
C21orf62	19743967
OLIG2	19976351
IFNAR2	20180297
IL10RB	20216777
IFNAR1	20275300
IFNGR2	20353293
C21orf4	20400614
C21orf55	20435928
GART	20453915
SON	20493461
ITSN1	20592797
ATP5O	20853849
MRPS6	21023940
SLC5A3	21045589
KCNE2	21314414
C21orf51	21325902
KCNE1	21399516
DSCR1	21466877
CLIC6	21658387
RUNX1	21738207
FLJ20856	21988335
C21orf18	22984669

SUR-ROUNDING GENE NAME	POSITION (bp)
CBR1	23020125
CBR3	23085092
C21orf5	23114668
KIAA0136	23270058
CHAF1B	23335222
CLDN14	23410443
PSMD4P	23435675
SIM2	23649498
HLCS	23703739
DSCR6	23955953
DSCR5	24015109
TTC3	24032681
DSCR3	24173160
DYRK1A	24368641
KCNJ6	24574220
DSCR4	25003750
DSCR8	25070978
KCNJ15	25206098
ERG	25329397
ETS2	25755188
DSCR2	26124818
WDR9	26135251
HMG14	26290570
WRB	26326951
SH3BGR	26392496
B3GALT5	26602941
DSCAM	27084862
BACE2	28110098
C21orf11	28259086
MX2	28312529
MX1	28368500
TMPRSS2	28406900

FIG.10

SUR-ROUNDING GENE NAME	DISTANCE FROM UNKNOWN GENE (bp)
C21orf42	24015
MRPL39	223832
JAM2	277456
ATP5J	362653
GABPA	367848
APP	518724
CYYR1	1104530
ADAMTS1	1474467
ADAMTS5	1559625
N6AMT1	3510598
ZNF294	3566241
C21orf6	3643855
USP16	3662745
CCT8	3694423
C21orf7	3714174
BACH1	3935542
NCAM2	4081218
GRIK1	4173600
CLDN17	4802605
CLDN8	4850668
TIAM1	5755089
SOD1	6296223
KIAA1172	6307651
HUNK	6509930
C21orf45	6905566
C21orf108	6947633
PRSS7	7007106
MGC14136	7029745
C21orf68	7031646
C21orf63	7049000
FLJ10932	7208852
C21orf59	7238412

SUR-ROUNDING GENE NAME	DISTANCE FROM UNKNOWN GENE (bp)
SYNJ1	7265376
C21orf66	7392956
C21orf62	7430178
C21orf91	7487501
OLIG2	7662562
BTG3	7682843
CXADR	7763468
IFNAR2	7866508
IL10RB	7902988
IFNAR1	7961511
IFNGR2	8039504
C21orf4	8086825
C21orf55	8122139
GART	8140126
SON	8179672
ITSN1	8279008
ATP5O	8540060
MRPS6	8710151
SLC5A3	8731800
KCNE2	9000625
C21orf51	9012113
KCNE1	9085727
DSCR1	9153088
CLIC6	9344598
RUNX1	9424418
USP25	9546285
FLJ20856	9674546
NRIP1	10315177
C21orf18	10670880
CBR1	10706336
CBR3	10771303
SAMSN1	10791168

SUR-ROUNDING GENE NAME	DISTANCE FROM UNKNOWN GENE (bp)
C21orf5	10800879
STCH	10903556
KIAA0136	10956269
ABCC13	11002598
CHAF1B	11021433
CLDN14	11096654
PSMD4P	11121886
SIM2	11335709
HLCS	11389950
DSCR6	11642164
DSCR5	11701320
TTC3	11718892
DSCR3	11859371
DYRK1A	12054852
KCNJ6	12260431
DSCR4	12689961
DSCR8	12757189
KCNJ15	12892309
ERG	13015608
ETS2	13441399
DSCR2	13811029
WDR9	13821462
HMG14	13976781
WRB	14013162
SH3BGR	14078707
B3GALT5	14289152
DSCAM	14771073
BACE2	15796309
C21orf11	15945297
MX2	15998740
MX1	16054711
TMPRSS2	16093111

FIG.11

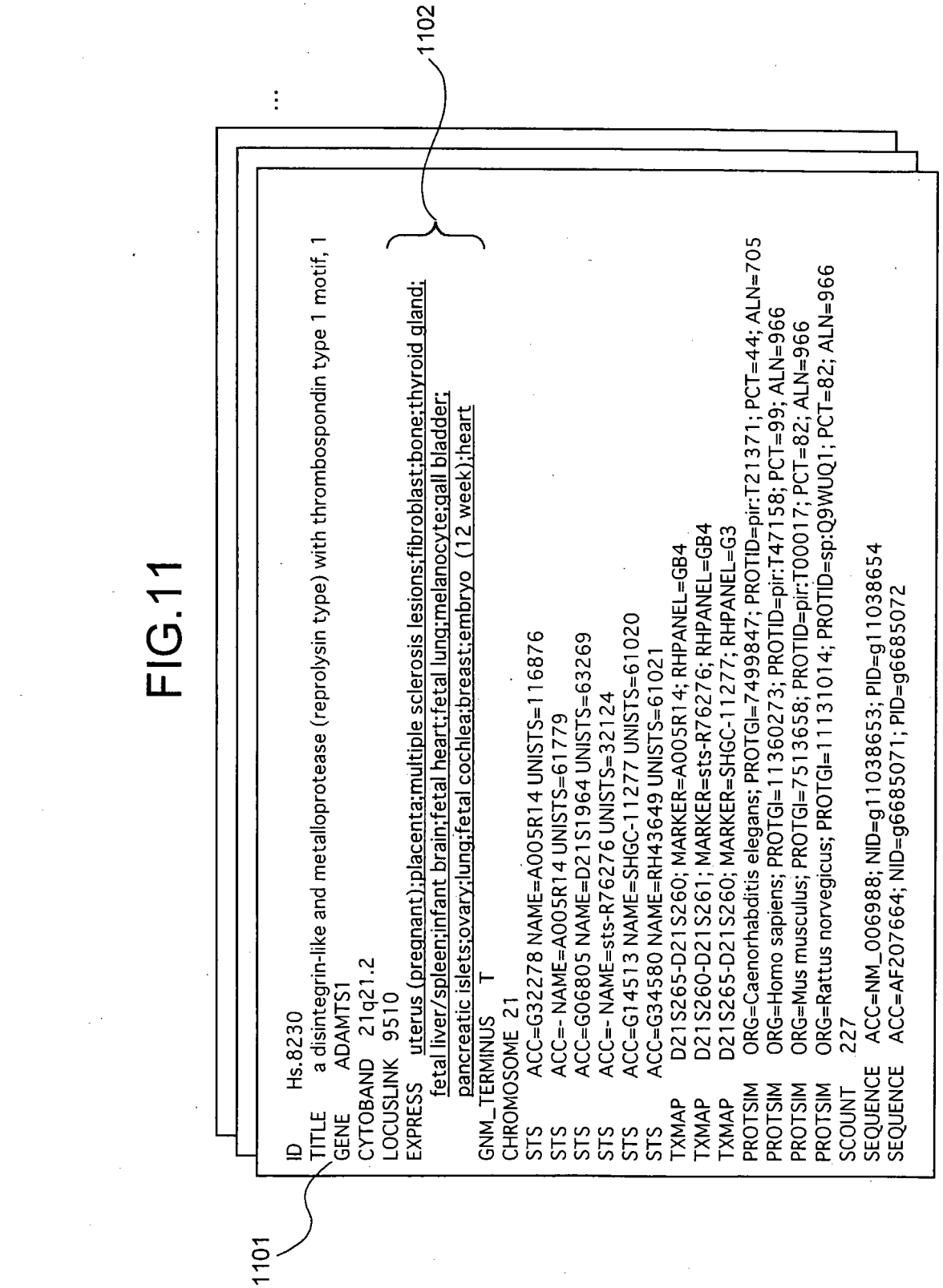
1101
1102
...
ID Hs.8230
TITLE a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 1
GENE ADAMTS1
CYTOBAND 21q21.2
LOCUSLINK 9510
EXPRESS uterus (pregnant);placenta;multiple sclerosis lesions;fibroblast;bone;thyroid gland;
fetal liver/spleen;infant brain;fetal heart;fetal lung;melanocyte;gall bladder;
pancreatic islets;ovary;lung;fetal cochlea;breast;embryo (12 week);heart
GNM_TERMINUS T
CHROMOSOME 21
STS ACC=G32278 NAME=A005R14 UNISTS=116876
STS ACC=- NAME=A005R14 UNISTS=61779
STS ACC=G06805 NAME=D21S1964 UNISTS=63269
STS ACC=- NAME=sts-R76276 UNISTS=32124
STS ACC=G14513 NAME=SHGC-11277 UNISTS=61020
STS ACC=G34580 NAME=RH43649 UNISTS=61021
TXMAP D21S265-D21S260; MARKER=A005R14; RHPANEL=GB4
TXMAP D21S260-D21S261; MARKER=sts-R76276; RHPANEL=GB4
TXMAP D21S265-D21S260; MARKER=SHGC-11277; RHPANEL=G3
PROTSIM ORG=Caenorhabditis elegans; PROTGI=7499847; PROTID=pir:T21371; PCT=44; ALN=705
PROTSIM ORG=Homo sapiens; PROTGI=11360273; PROTID=pir:T47158; PCT=99; ALN=966
PROTSIM ORG=Mus musculus; PROTGI=7513658; PROTID=pir:T00017; PCT=82; ALN=966
PROTSIM ORG=Rattus norvegicus; PROTGI=11131014; PROTID=sp:Q9WUQ1; PCT=82; ALN=966
SCOUNT 227
SEQUENCE ACC=NM_006988; NID=g11038653; PID=g11038654
SEQUENCE ACC=AF207664; NID=g6685071; PID=g6685072

FIG.12

SURROUNDING GENE NAME	EXPRESSION SITE
C21orf42	brain;germ cell;lymphoma, cell line;pool;testis
MRPL39	Stomach;adenocarcinoma;adrenal gland;blood;brain;breast;carcinoma, cell line;cervical carcinoma cell line ;chondrosarcoma;choriocarcinoma;colon;denis_drash;duodenal adenocarcinoma, cell line;fetal eyes;fetal eyes, lens, eye anterior segment, optic nerve, retina, retina foveal and macular, rpe and choroid;foreskin;from chronic myelogenous leukemia;glioblastoma;glioblastoma with egfr amplification;head_neck;head_normal;heart;hippocampus, cell line;hypothalamus, cell line;kidney;leiomyosarcoma;liver;lung;lung_normal;melanoma (mewo cell line);melanotic melanoma;neuroblastoma;ovary;parathyroid;placenta;pool;pooled;primitive neuroectoderm;prostate;retina foveal and macular;rhabdomyosarcoma;testis;thymus, pooled;tonsil;uterus;whole embryo
JAM2	brain;carcinoid;ear;fetal eye;germ cell;glioblastoma;glioblastoma with egfr amplification;heart;hypothalamus, cell line;kidney;lung;lung_normal;nervous_normal;nervous_tumor;neuroblastoma cells;neuroblastoma, cell line;ovary (pool of 3);pancreas;placenta;pool;pooled;pooled brain, lung, testis;prostate;retina foveal and macular;rpe and choroid;subchondral bone;testis;testis, cell line;testis_normal;three pooled meningiomas;uterus
ATP5J	Stomach;adenocarcinoma;adrenal cortex carcinoma, cell line;adrenal cortico adenoma for cushing's syndrome;adrenal gland;aorta;ascites;bladder_tumor;blood;bone;bone marrow;brain;breast;carcinoid;carcinoma, cell line;colon;colon_normal;cord blood;correspond
GABPA	Stomach;adenocarcinoma;amygdala;blood;brain;breast_normal;carcinoid;cns;colon;duodenal adenocarcinoma, cell line;embryonal carcinoma;embryonal carcinoma, cell line;foreskin;germ cell;head_neck;heart;hippocampus, cell line;kidney;leiomyosarcoma;lung;lymphoma, cell line;mammary adenocarcinoma, cell line;medulla;neuroblastoma cells;ovary;placenta;pool;retinoblastoma;small intestine;testis;uterus
APP	2 pooled high-grade transitional cell tumors;2 pooled wilms' tumors, one primary and one metastatic to brain;Fetal brain;Prostate;Stomach;adenocarcinoma;adenocarcinoma cell line;adenocarcinoma,
CYYR1	2 pooled wilms' tumors, one primary and one metastatic to brain;adrenal gland;brain;breast;breast_normal;carcinoid;chondrosarcoma;cns;follicular carcinoma;from acute myelogenous leukemia;hepatocellular carcinoma;insulinoma;kidney;lung;metastatic chondrosarcoma;ovary (pool of 3);parathyroid;pool;pooled;prostate;testis_normal;uterus;whole embryo

FIG.13

SURROUNDING GENE NAME	EXPRESSION SITE
C21orf42	brain;germ cell;lymphoma, cell line;pool;testis
MRPL39	Stomach;adenocarcinoma;adrenal gland;blood;breast;carcinoma, cell line;cervical carcinoma cell line;chondrosarcoma;choriocarcinoma;colon;denis_drash;duodenal adenocarcinoma, cell line;fetal eyes;fetal eyes, lens, eye anterior segment, optic nerve, retina, retina foveal and macular, rpe and choroid;foreskin;from chronic myelogenous leukemia;glioblastoma;glioblastoma with egfr amplification;head_neck;head_normal;heart;hippocampus, cell line;hypothalamus, cell line;kidney;leiomyosarcoma;liver;lung;lung_normal;melanoma (mewo cell line);melanotic melanoma;neuroblastoma;ovary;parathyroid;placenta;pooled;primitive neuroectoderm;prostate;retina foveal and macular;rhabdomyosarcoma;thymus, pooled;tonsil;uterus;whole embryo
JAM2	carcinoid;ear;fetal eye;nervous_normal;nervous_tumor;neuroblastoma cells;neuroblastoma, cell line;ovary (pool of 3);pancreas;pooled brain, lung, testis;rpe and choroid;subchondral bone;testis, cell line;testis_normal;three pooled meningiomas
ATP5J	adrenal cortex carcinoma, cell line;adrenal cortico adenoma for cushing's syndrome;aorta;ascites;bladder_tumor;bone;bone marrow;colon_normal;cord blood;correspond
GABPA	amygdala;breast_normal;cns;embryonal carcinoma;embryonal carcinoma, cell line;mammary adenocarcinoma, cell line;medulla;retinoblastoma;small intestine
APP	2 pooled high-grade transitional cell tumors;2 pooled wilms' tumors, one primary and one metastatic to brain;Fetal brain;Prostate;adenocarcinoma cell line;adenocarcinoma, cell line;adipose;adrena
CYYR1	follicular carcinoma;from acute myelogenous leukemia;hepatocellular carcinoma;insulinoma;metastatic chondrosarcoma
ADAMTS1	amnion_normal;colonic mucosa from 3 patients with crohn's disease;duodenal adenocarcinom
ADAMTS5	muscle

FIG.14

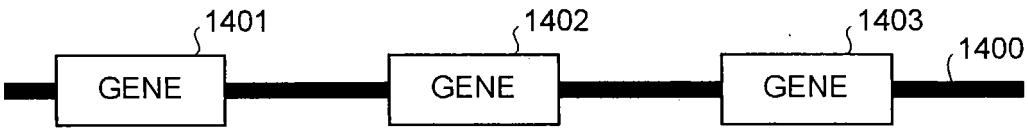

FIG.15

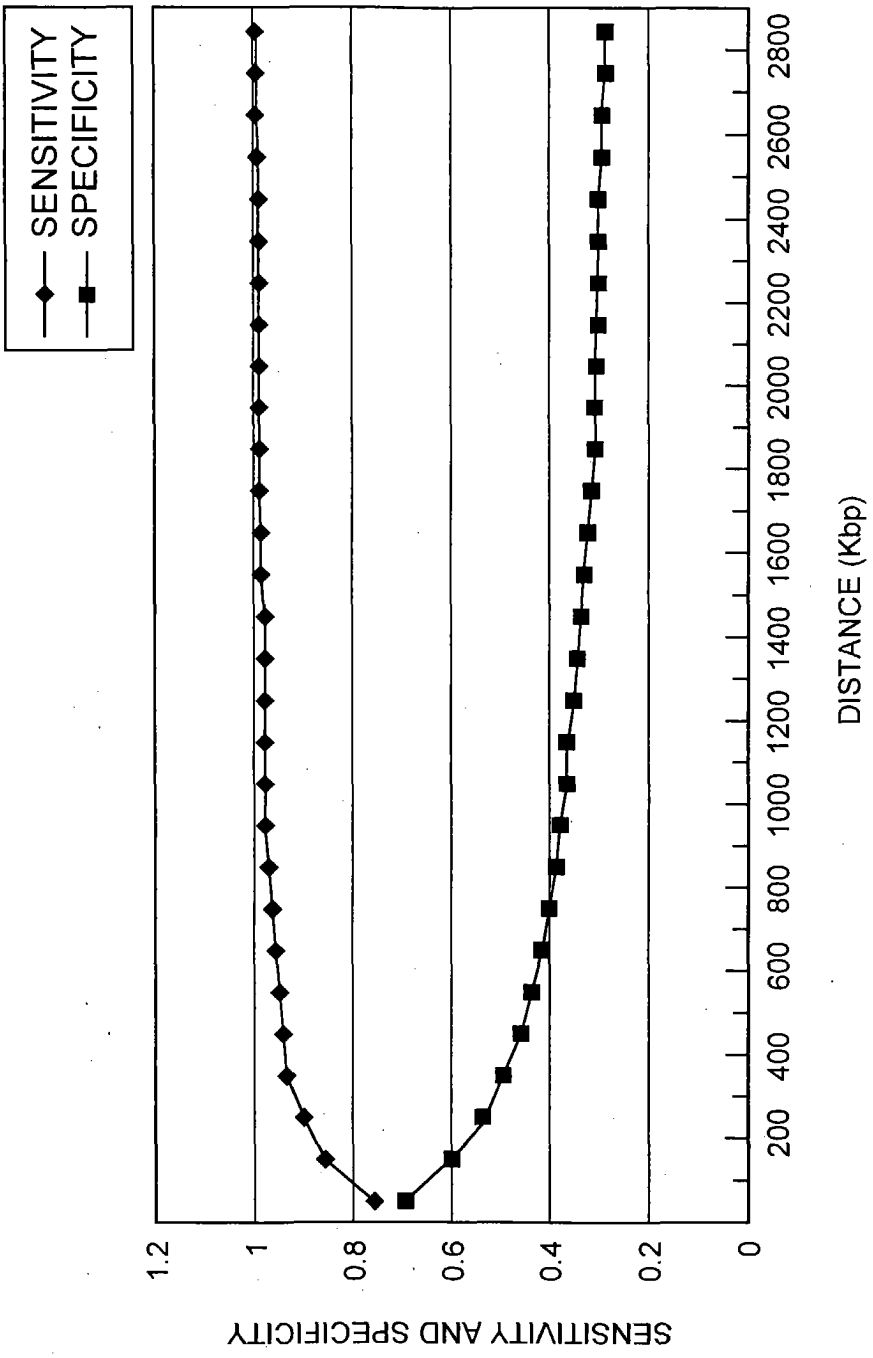
SENSITIVITY
SPECIFICITY
SENSITIVITY AND SPECIFICITY
1.2
1
0.8
0.6
0.4
0.2
0
200 400 600 800 1000 1200 1400 1600 1800 2000 2200 2400 2600 2800
DISTANCE (Kbp)

FIG.16

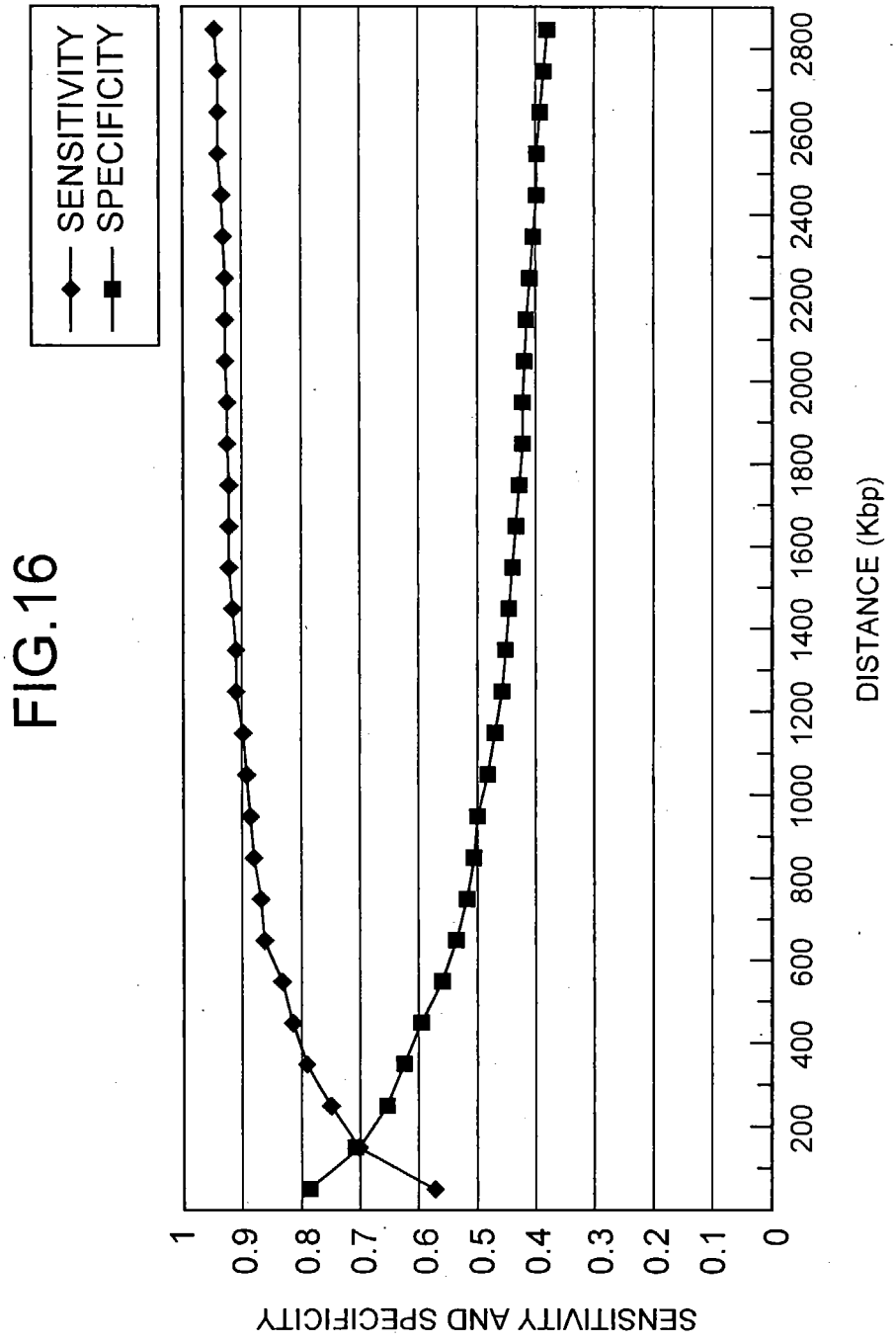
SENSITIVITY
SPECIFICITY
SENSITIVITY AND SPECIFICITY
0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1
200
400
600
800
1000
1200
1400
1600
1800
2000
2200
2400
2600
2800
DISTANCE (Kbp)

FIG.17

SURROUNDING GENE NAME	EXPRESSION SITE
STCH	kidney; 2 pooled tumors (clear cell type); leukopheresis; hippocampus; large cell carcinoma; placenta; chondrosarcoma grade ii; neuroblastoma cells; cornea; mucoepidermoid carcinoma; liver; aorta; serous papillary carcinoma, high grade, 2 pooled tumors; pineal gland; retinoblastoma; glioblastoma with egfr amplification; cervix; embryonal carcinoma, cell line; 2 pooled wilms' tumors, one primary and one metastatic to brain; melanotic melanoma; embryo, 8 weeks; alveolar rhabdomyosarcoma; leiomyosarcoma; b-cell, chronic lymphotic leukemia; retina; primitive neuroectoderm; duodenal adenocarcinoma, cell line; germinal center b cell; brain; rpe/choroid; muscle (skeletal); colon; adrenal cortex carcinoma, cell line; pooled; metastatic chondrosarcoma; carcinoid; marrow; adenocarcinoma; islets of langerhans; breast_normal; moderately-differentiated adenocarcinoma; lymph; mixed (pool of 40 rnas); cervical carcinoma cell line; cartilage; chondrosarcoma; pooled germ cell tumors; colon_ins; hypernephroma; osteosarcoma, cell line; metastatic prostate bone lesion; prostate; embryo; testis; large cell carcinoma, undifferentiated; pineal body; carcinoma, cell line; human skeletal muscle; whole embryo, mainly body; uterus; cell lines; liver and spleen; transitional cell papilloma, cell line; anaplastic oligodendroglioma with 1p/19q loss; breast; whole brain; three pooled meningiomas; fetal eyes, lens, eye anterior segment, optic nerve, retina, retina foveal and macular, rpe and choroid; ovary; from chronic myelogenous leukemia; melanotic melanoma, high mdr; insulinoma; ascites; pooled human melanocyte, fetal heart, and pregnant uterus; lung
RBM11	hypothalamus; multiple sclerosis lesions; ewing's sarcoma
SAMSN1	aveolar macrophage; moderately-differentiated endometrial adenocarcinoma, 3 pooled tumors; cochlea; stomach; from acute myelogenous leukemia; pheochromocytoma; heart; lymphoma, cell line; renal cell tumor; lymphoma, follicular mixed small and large cell; blood; bone marrow; myeloid cells, 18 pooled cml cases, bcr/abl rearrangement positive, includes both chronic phase and myeloid blast crisis

1701

FIG.18

SURROUNDING GENE NAME	EXPRESSION SITE
CD22	lymph; leukopheresis; chondrosarcoma; pooled pancreas and spleen; pooled germ cell tumors; mixed; placenta_normal; pooled lung and spleen; eye; serous papillary carcinoma, high grade, 2 pooled tumors; prostate; large cell carcinoma, undifferentiated; embryonal carcinoma, cell line; leukocyte; multiple sclerosis lesions; melanotic melanoma; prostate_normal; b-cell, chronic lymphotic leukemia; nervous_tumor; nervous_normal; burkitt lymphoma; primary b-cells from tonsils (cell line); testis_normal; germinal center b cell; lymphoma, cell line; spleen; pooled; metastatic chondrosarcoma; lymphoma, follicular mixed small and large cell; purified pancreatic islet; denis_drash; marrow; adenocarcinoma; b cells from burkitt lymphoma; head_neck
GPR41	ovary (pool of 3)
FLJ22814	lung
MAG	dorsal root ganglia; tumor, 5 pooled (see description); hypothalamus; brain; pooled brain, lung, testis; hippocampus; t cells from t cell leukemia; whole brain; anaplastic oligodendroglioma; sympathetic trunk; total brain; optic nerve
HAMP	mixed (pool of 40 rnas); fetal eyes, lens, eye anterior segment, optic nerve, retina, retina foveal and macular, rpe and choroid; squamous cell carcinoma, poorly differentiated (4 pooled tumors, including primary and metastatic); fetal spleen; liver

FIG.19

SURROUNDING GENE NAME	EXPRESSION SITE
USF2	kidney; neuroblastoma; 2 pooled tumors (clear cell type); astrocytoma grade iv, cell line; human lung epithelial cells; adenocarcinoma, cell line; melanotic melanoma, cell line; lung normal; large cell carcinoma; subchondral bone; placenta; natural killer cells, cell line; neuroblastoma cells; hypernephroma, cell line; 2 pooled high-grade transitional cell tumors; glioblastoma with egfr amplification; retinoblastoma; human retina; prostatic intraepithelial neoplasia - high grade; myeloma; prostate_tumor; leiomyosarcoma; lung_tumor; duodenal adenocarcinoma, cell line; adenocarcinoma cell line; head_normal; colon; epithelioid carcinoma cell line; small cell carcinoma; epid_tumor; rpe and choroid; well-differentiated endometrial adenocarcinoma, 7 pooled tumors; carcinoid; squamous cell carcinoma; epidermoid carcinoma, cell line; islets of langerhans; rhabdomyosarcoma; glioblastoma; normal prostatic epithelial cells; epithelioid carcinoma; schizophrenic brain s-11 frontal lobe; stomach; ductal carcinoma, cell line; cervical carcinoma cell line; amelanotic melanoma, cell line; renal cell tumor; colon_ins; glioblastoma (pooled); adrenal gland; fetal eye; pooled colon, kidney, stomach; pectoral muscle (after mastectomy); embryo; normal prostate; enchondroma cell line; melanocyte; skin; lens; uterus; liposarcoma; cell lines; liver and spleen; transitional cell papilloma, cell line; glioblastoma with probably tp53 mutation and without egfr amplification; anaplastic oligodendroglioma with 1p/19q loss; endometrium, adenocarcinoma cell line; breast; iris; colonic mucosa from 3 patients with crohn's disease; ovary; medulla; ascites
LISCH7	choriocarcinoma; heart; pancreas; germ cell tumor; cervix; retina; moderately-differentiated endometrial adenocarcinoma, 3 pooled tumors; primary lung epithelial cells; renal cell adenocarcinoma; primary lung cystic fibrosis epithelial cells; adrenal cortex carcinoma, cell line; hepatocellular carcinoma, cell line; poorly differentiated adenocarcinoma with signet ring cell features; moderately-differentiated adenocarcinoma; uterine; tumor; testis; moderately differentiated adenocarcinoma; carcinoma, cell line; poorly-differentiated endometrial adenocarcinoma, 2 pooled tumors; normal endometrium, mid-secretory phase, cycle day 23; teratocarcinoma, cell line; three pooled meningiomas; lymph node; colon_normal; colon tumor, rer+; two pooled squamous cell carcinomas

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